

Membrane Protein Structure

A Role for The APS

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APS Workshop on Membrane Science, ANL. August 2004

Overview

♣ **Membranes**

♣ **Structure - Function**

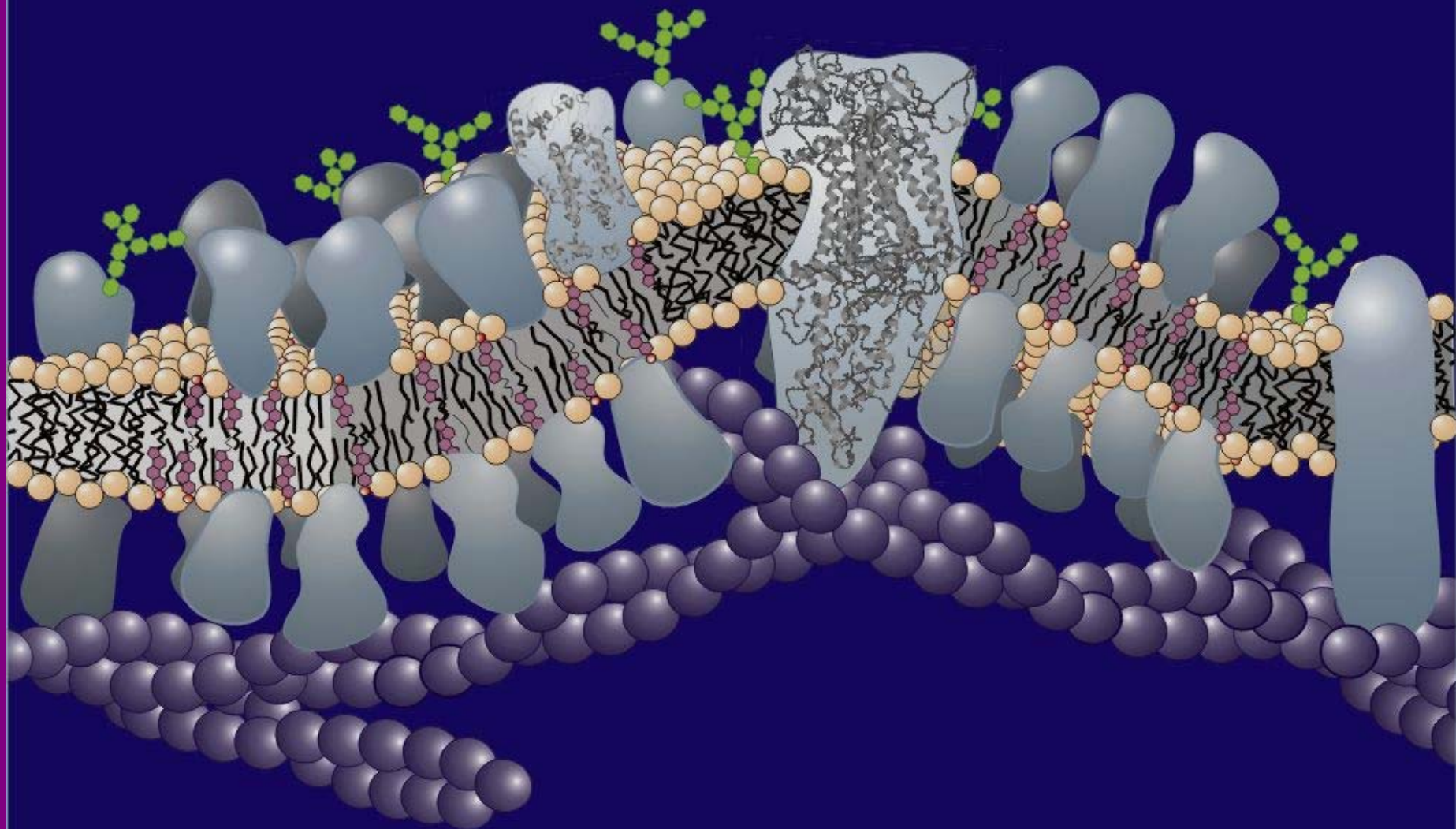
♣ **Bottleneck #1: Production**

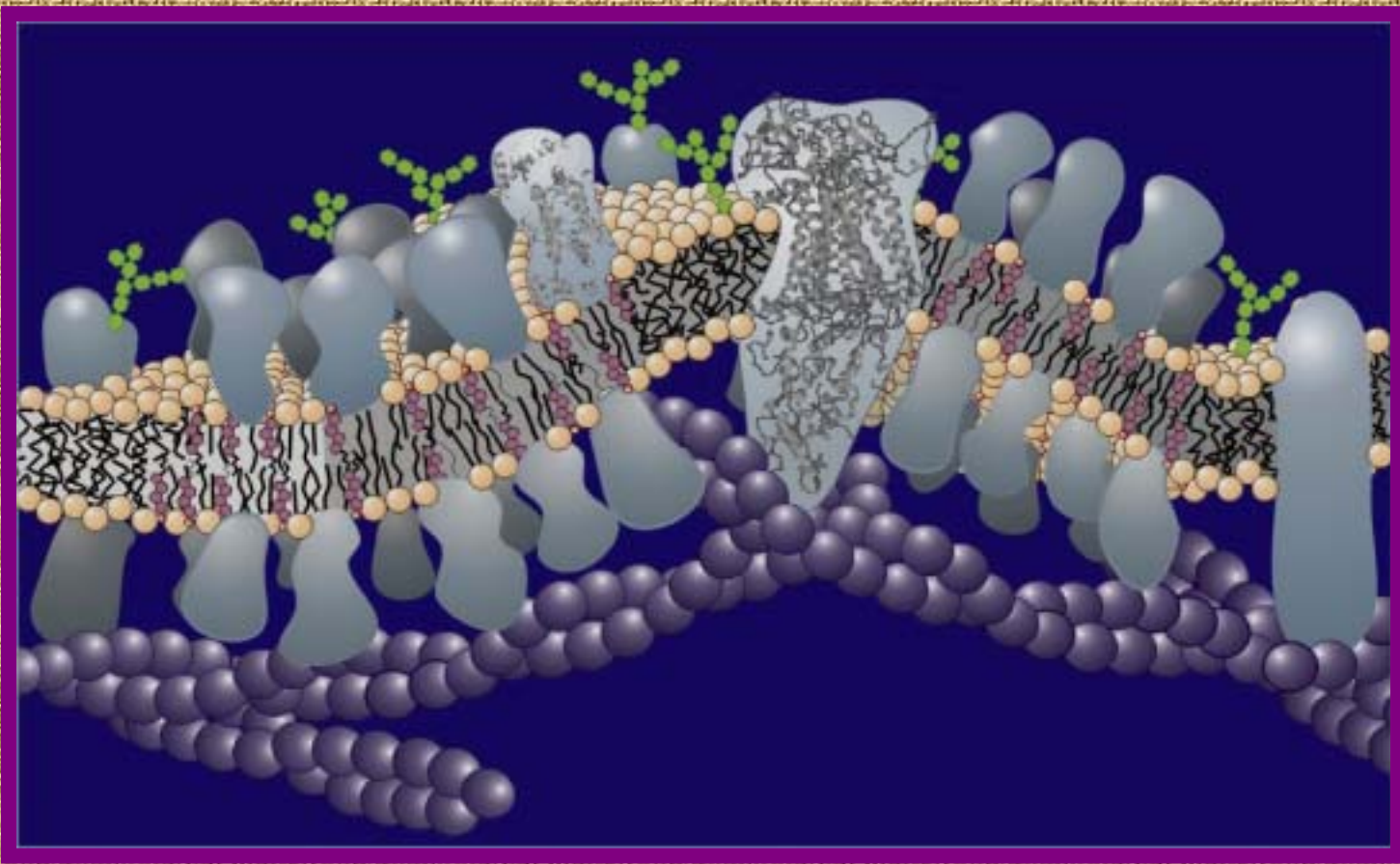
♣ **Bottleneck #2: Crystallization**

♣ ***In meso* Robot**

♣ **APS**







Functions

Health significance: senses (sight, touch, hearing, smell, taste)

Aberrations: senses, cystic fibrosis, GPCRs, drug delivery, drug sensitivity/resistance, trafficking, Parkinson's, pain.

Overview

♣ Membranes

♣ Structure - Function

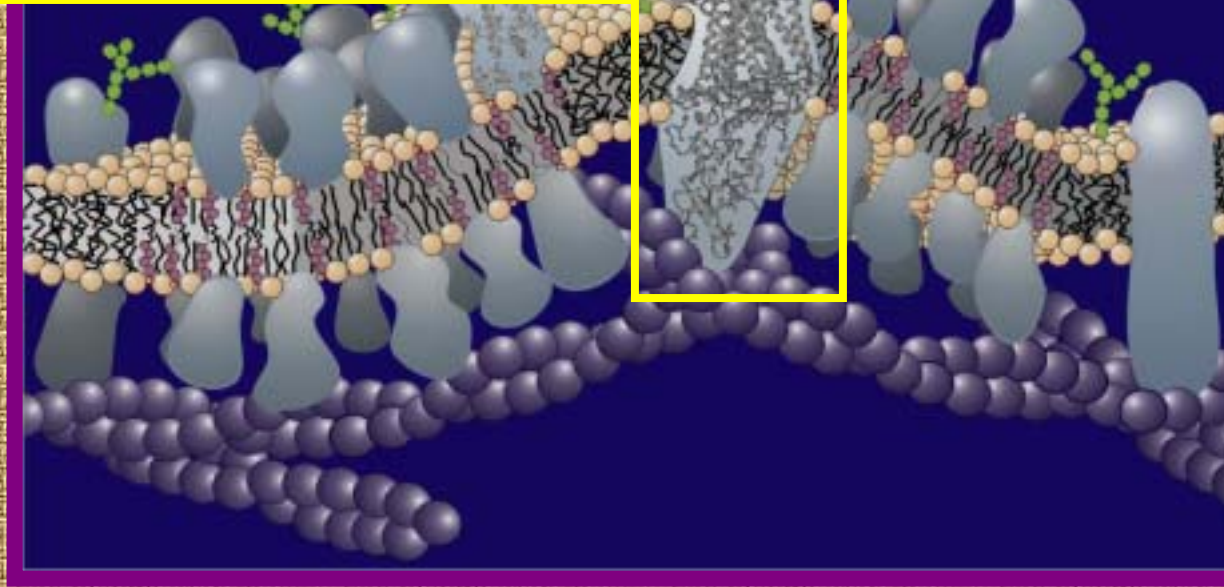
♣ Bottleneck #1: Production

♣ Bottleneck #2: Crystallization

♣ *In meso* Robot

♣ APS

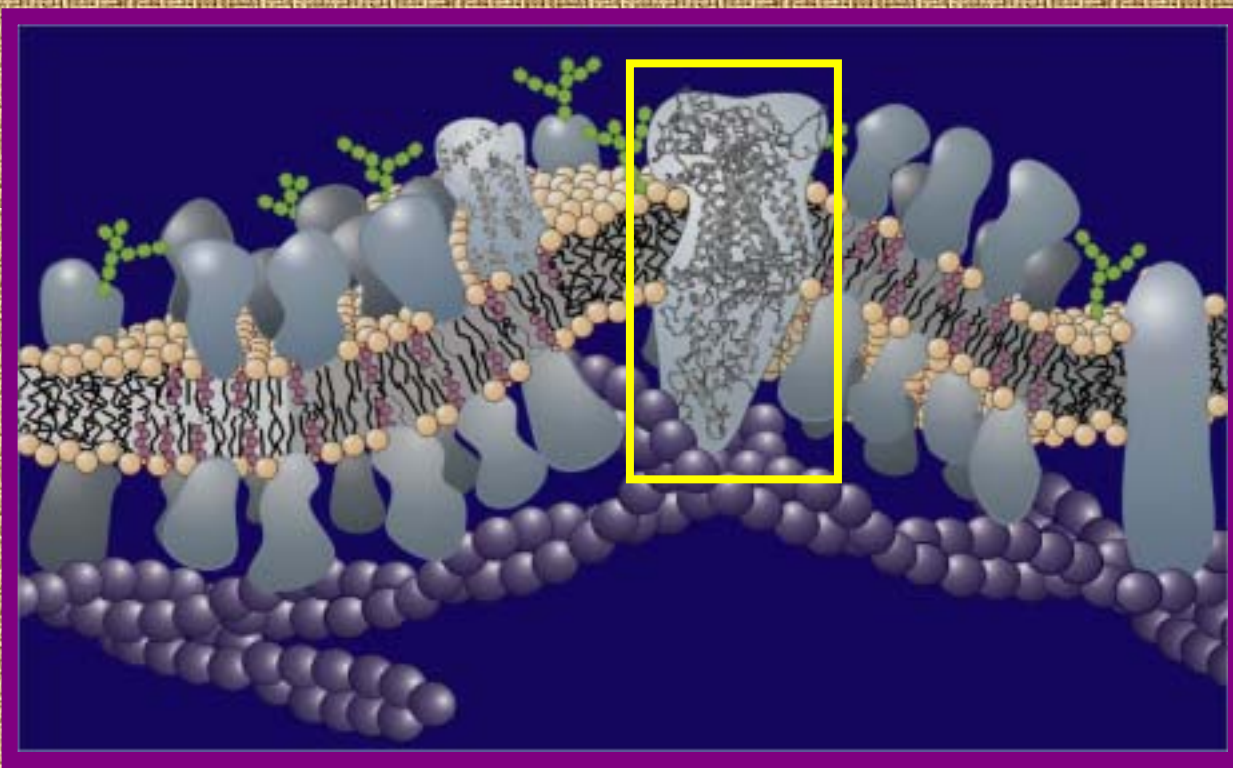
Membrane Protein Structure



Grand Challenge: *structure dictates function*

Basic knowledge and understanding
Rational design and exploitation
Prevention, treatment, repair

APS contribution: structure via MX



NIH. Human genome project. Structural genomics
‘Challenging Proteins’ - membrane proteins, complexes and human proteins
Protein Structure Initiative-2: 200 structures/yr @ \$50k/structure
Systematic studies to miniaturize, automate, HTP, reduce cost.
APS must prepare for the onslaught.

Beam time needs \propto (# samples / useful dataset) (etc.)

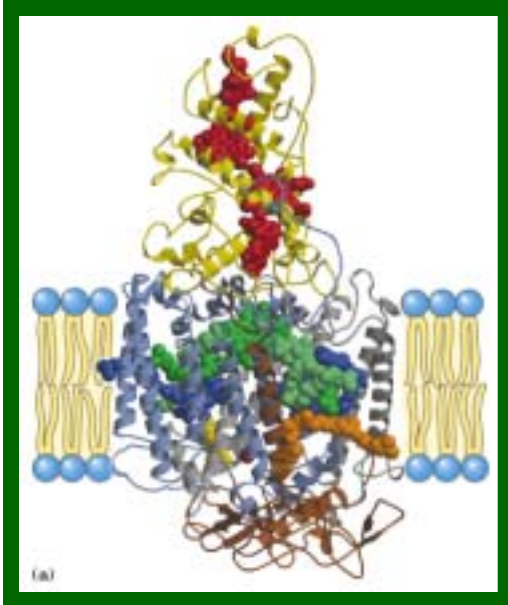
Low *versus* high hanging fruit



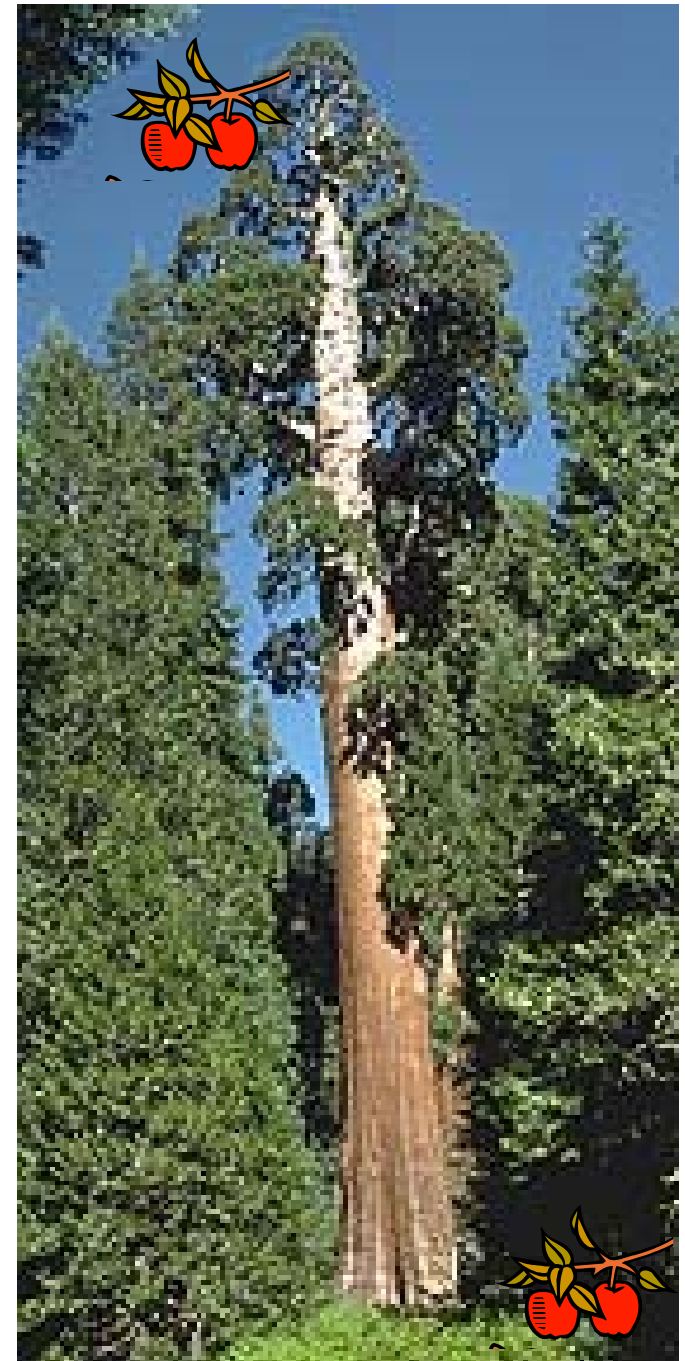
Low *versus* high hanging fruit

Membrane Proteins represent
The Giant Sequoia

- Amphipathic
- Flexible – transport
- Low-abundance



Lots



The Numbers Game

27 % of ORF in sequenced genomes code for integral membrane proteins

Human Genome: 30,000 - 50,000

Numbers are large

Head start: ~25 unique known structures
- PDB

To work down the deficit

Diffraction-Quality Crystals

2 Major Challenges

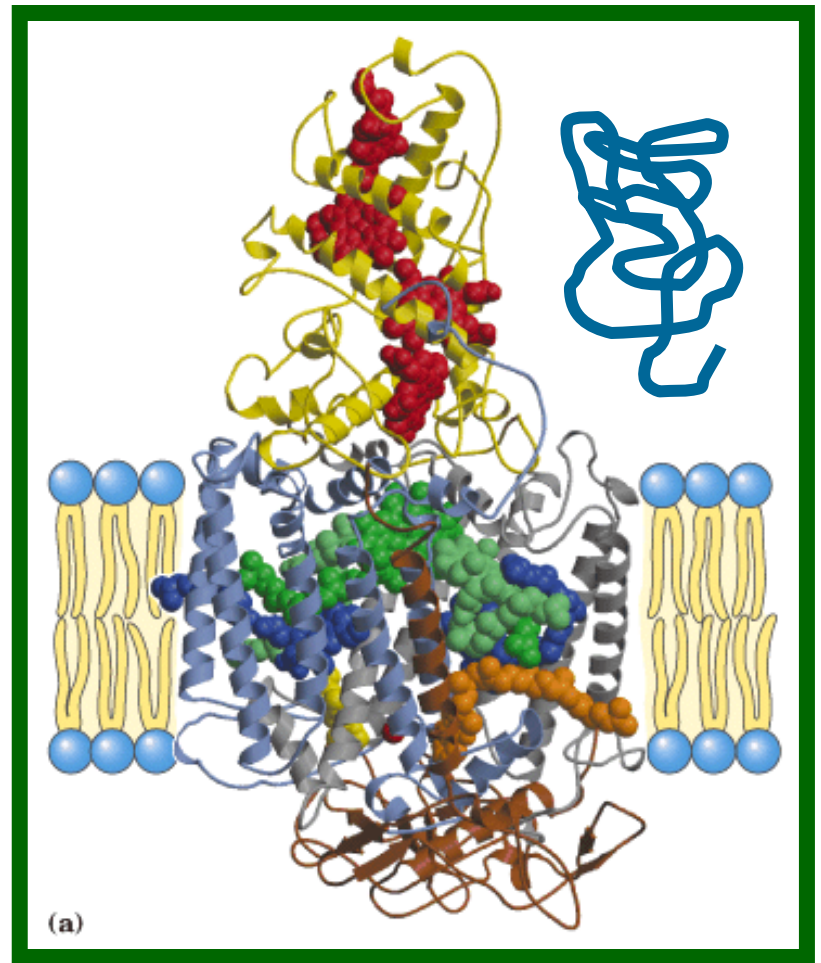
Protein

Crystal

Produce

Solubilize / purify / (refold / stabilize / reconstitute)

Crystallize



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♣ *In meso* Robot

♣ **APS**

Mammalian Protein Production

Yield	Pure	Homogenous	Structure-grade	Functional
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Natural sources: Muscle, Eye, Heart, RBC, e-Organ

Prokaryotes: *E. coli*, *L. lactis*

Eukaryotes: Yeast: *S. cervicia*, *Pichia*

Mammalian: Lots, HEK293, \pm GnT1⁻, suspension

Complex, expensive, but has what it takes

Cell-free, *In vitro*: *E. coli*, wheat germ

Expensive, advantages, high-risk/payoff

Others: Algae (*chlorella*), caterpillars, Baculovirus/Sf# Insect

Challenges

Heterologous Expression

(CFTR in *E. coli* or yeast)

Lots but **insoluble**, inclusion bodies, that may or may not **refold**

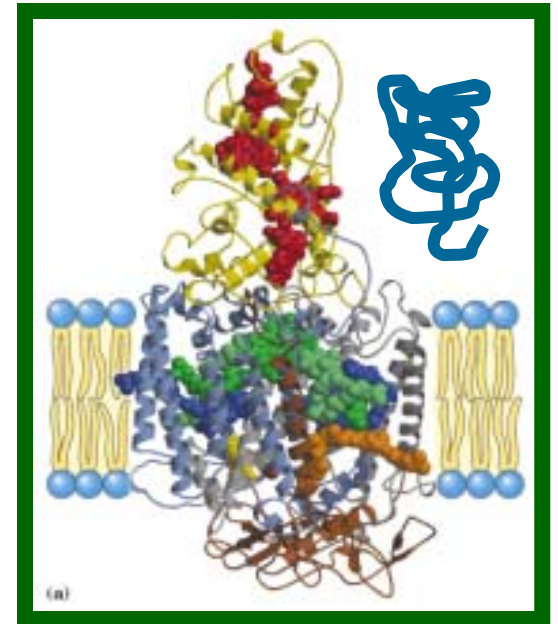
or

improperly folded in host membrane
non-functional (alien lipid profile)

and/or

not **post-translationally modified** correctly (sugar, lipid, clipping, -SS-)

Co-express/Engg chaperones, folding/trafficking enzymes, signal sequences, membrane proliferation, mutate for stability/crystallizability.



Solubilize Purify Refold Stabilize Reconstitute

Typically **detergent**, possibly other **small molecules**, **thousands** to choose from, **no rules**. Use the one in which protein is **stable**. **Screen** for solubilization, stabilization, crystallizability

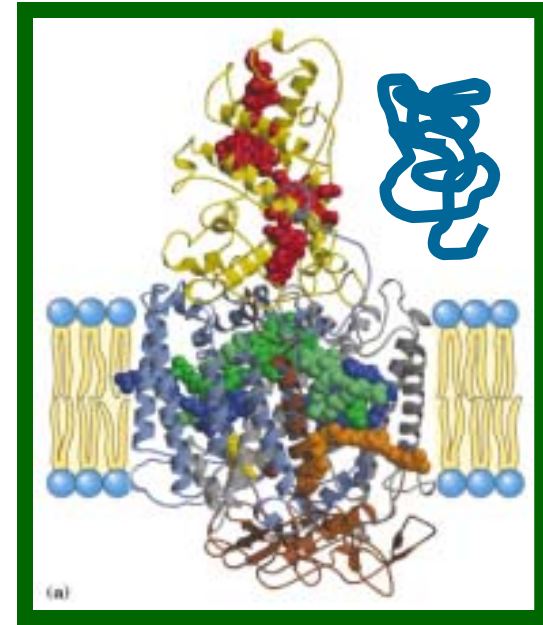
May need a **mix** of detergents, small molecules, bridging ions

May need **one detergent for purification**
another for stability/cost, exchange

Purification Tags for affinity chromatography.

N-, C-, internal, screen. Types His, Flag, fusion MBP, Antibodies
Screen for +/- retention for crystal structure determination

Purify, but not to death !



Overview

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♣ **Bottleneck #2: Crystallization**

♣ *In meso* Robot

♣ **APS**

Crystallogenesi

Crystallizability a part of **Quality Control** and a **Conduit to Structure**.

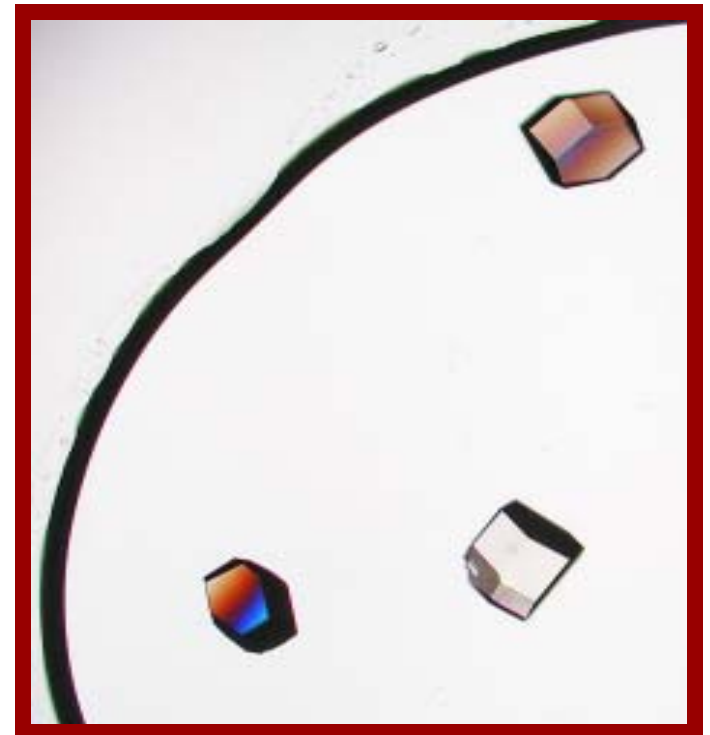
Measure of: **yield, purity, structural and chemical homogeneity**

functional ?

– no guarantee!

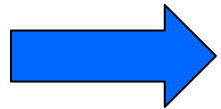
Diffraction Quality

– **Structure-grade ?**



Methods for Crystallizing Membrane Proteins

♣ *In surfo*



♣ *In meso* (*cubo*, vesicle, bicelle)

♣ Jig - saw

♣ Bypass

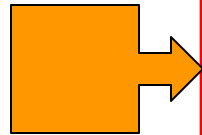
♣ Ax

♣ Wetting ?

LIQUID

LIQUID CRYSTALLINE

Fluid isotropic
FI



Lamellar crystal
 L_c



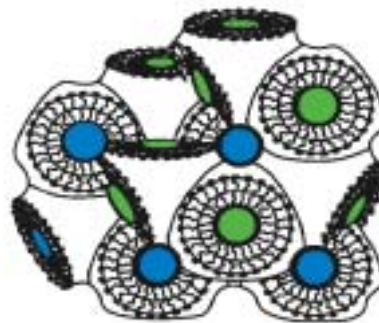
Lamellar
liquid crystal
 L_α



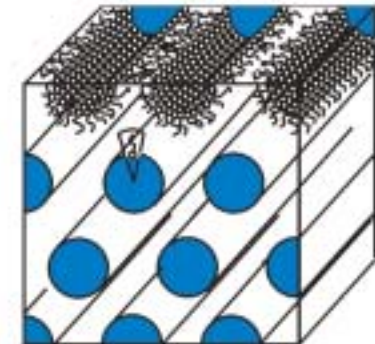
Biomembrane



Cubic
 $Pn3m$



Inverted hexagonal
 H_{II}

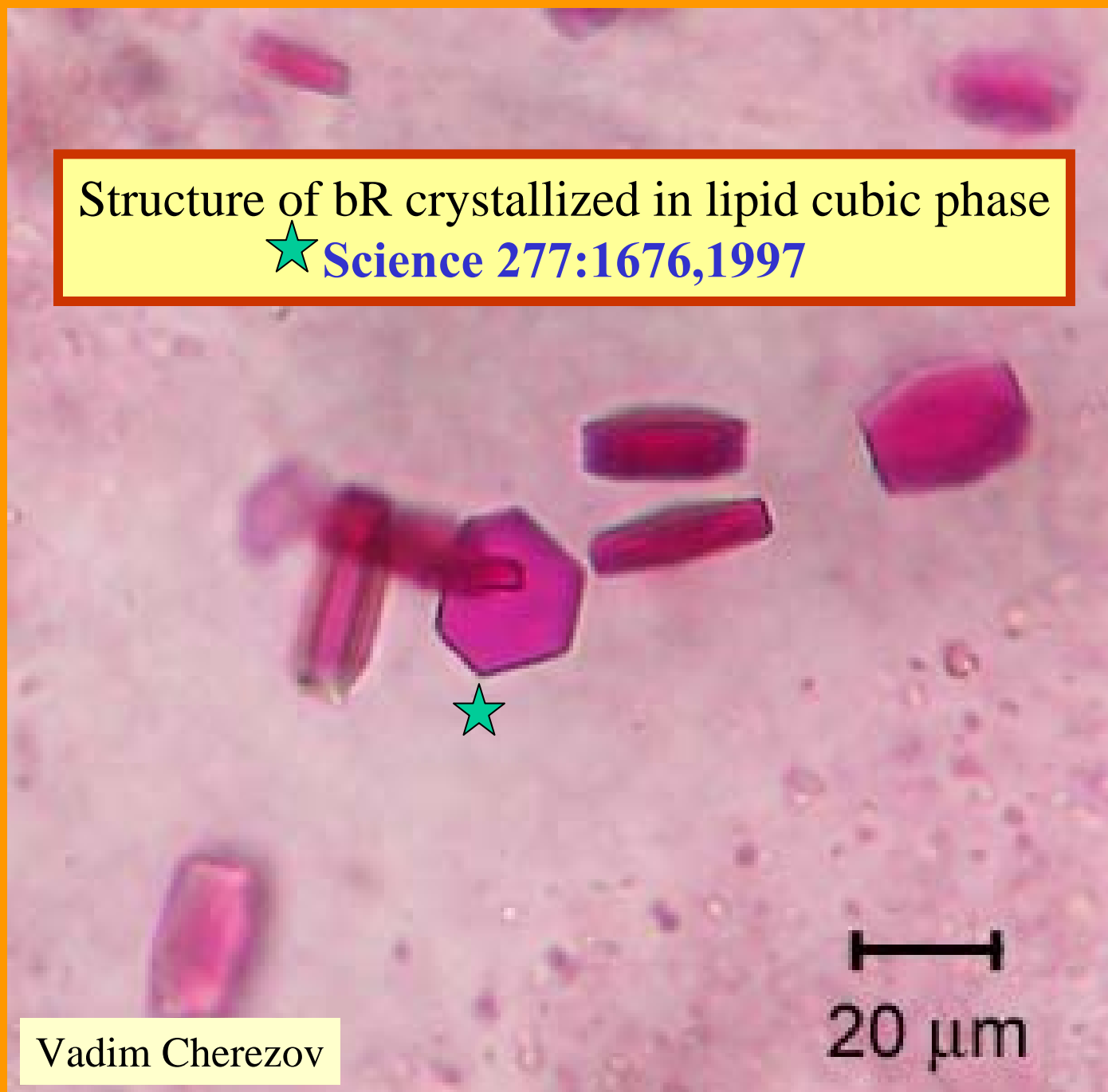


SOLID

mesophases

Structure of bR crystallized in lipid cubic phase

★ **Science 277:1676,1997**



Vadim Cherezov

**Lamellar
portal**

**Protein
co-crystal**

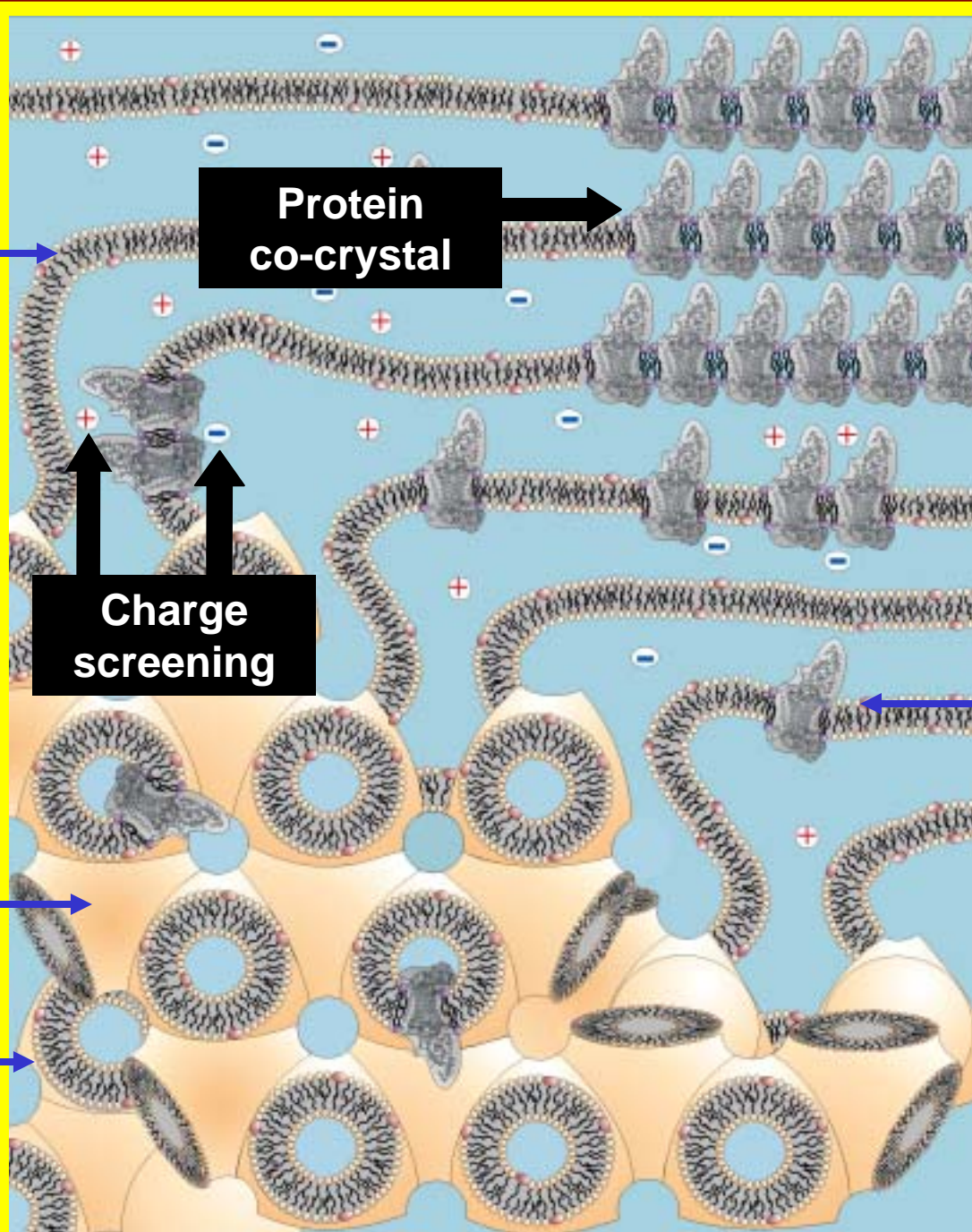
**Crystalline
array**

**Charge
screening**

**Reconstituted
protein**

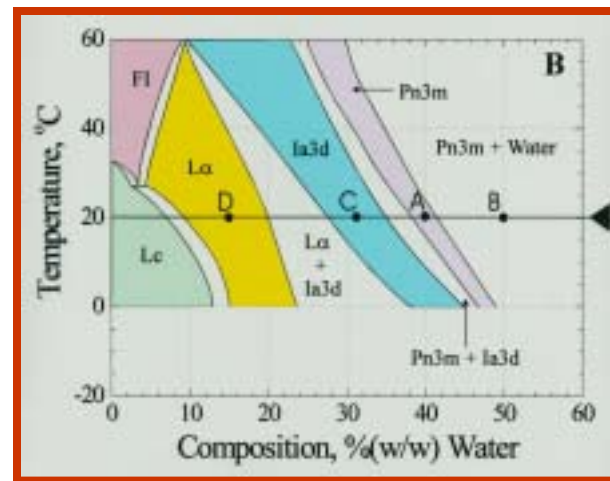
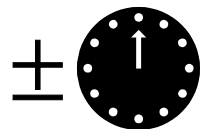
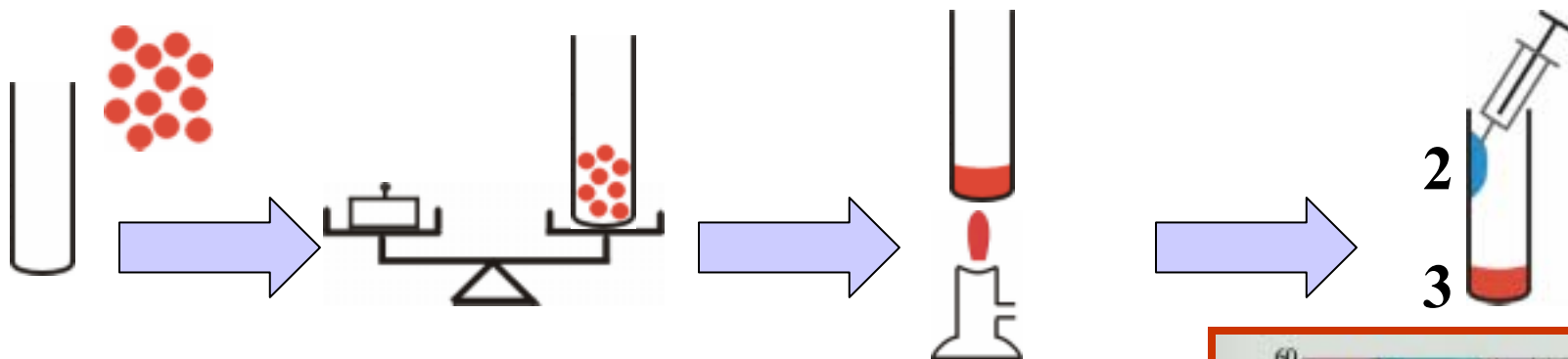
**Cubic
phase**

Lipids

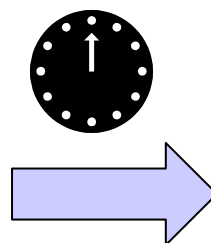
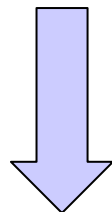


**J. Struct. Biol.
142:108-132**

The Original Method



≥ 1 hour
per 5 mg
Sample



Overview

- ♣ Membranes
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- ♣ Bottleneck #1: Production
- ♣ Bottleneck #2: Crystallization
- ♣ ***In meso* Robot: Miniaturize, Auto, HTP, Cost**
- ♣ **APS**

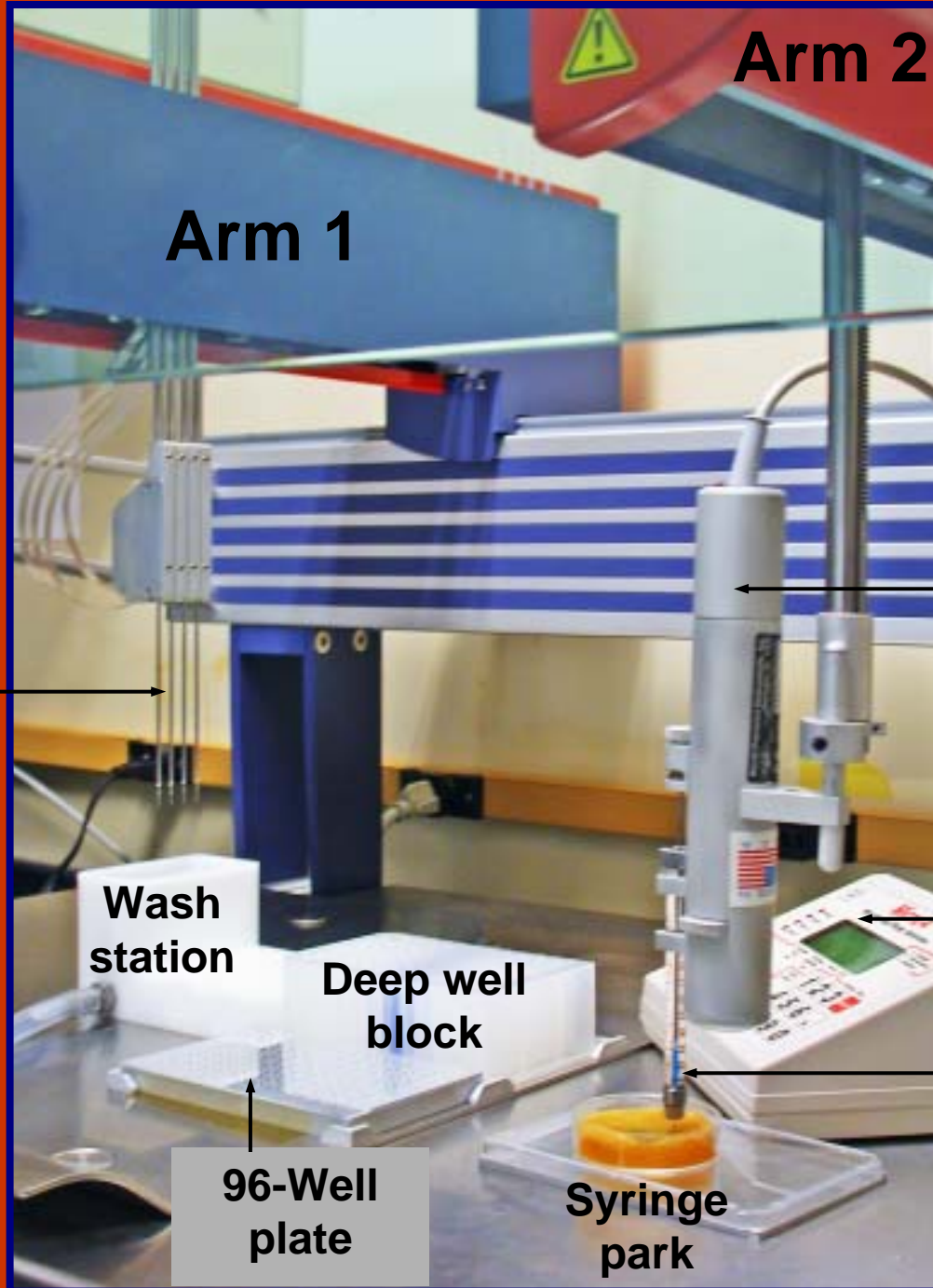
In Meso Robot

Liquid
Handling
Robot

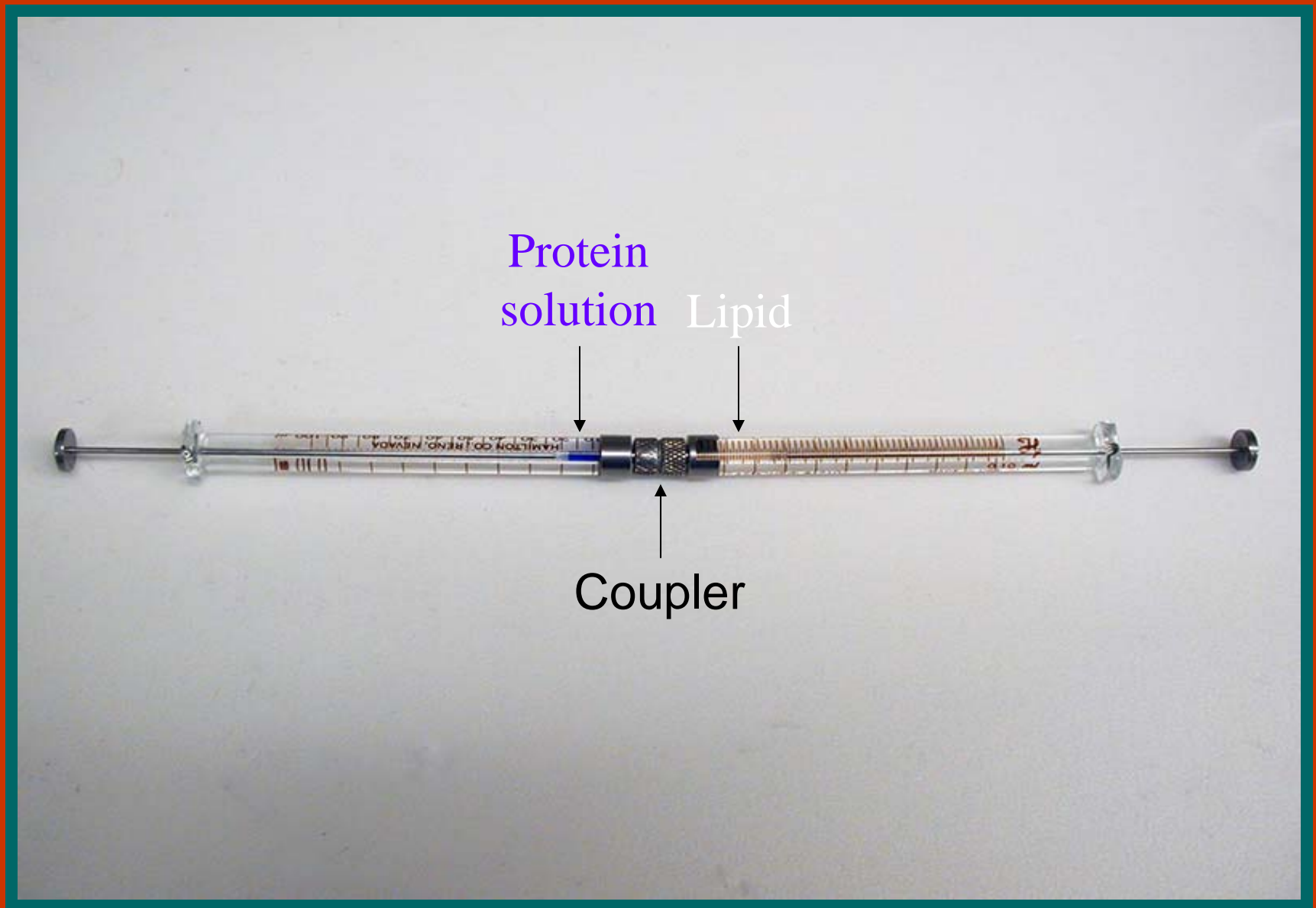
4-Tip
precipitant
solution
dispenser

Motorized
Micro-pump

Acta D. In press



Step-by-Step Use of the *In Meso* Robot



Syringe Mixer containing blue membrane protein solution in the syringe on the left and lipid in syringe on the right. Ratio of lipid to protein solution is ~ 3 / 2 by vol.



Mechanically mixing the protein solution and lipid together to form the cubic mesophase.

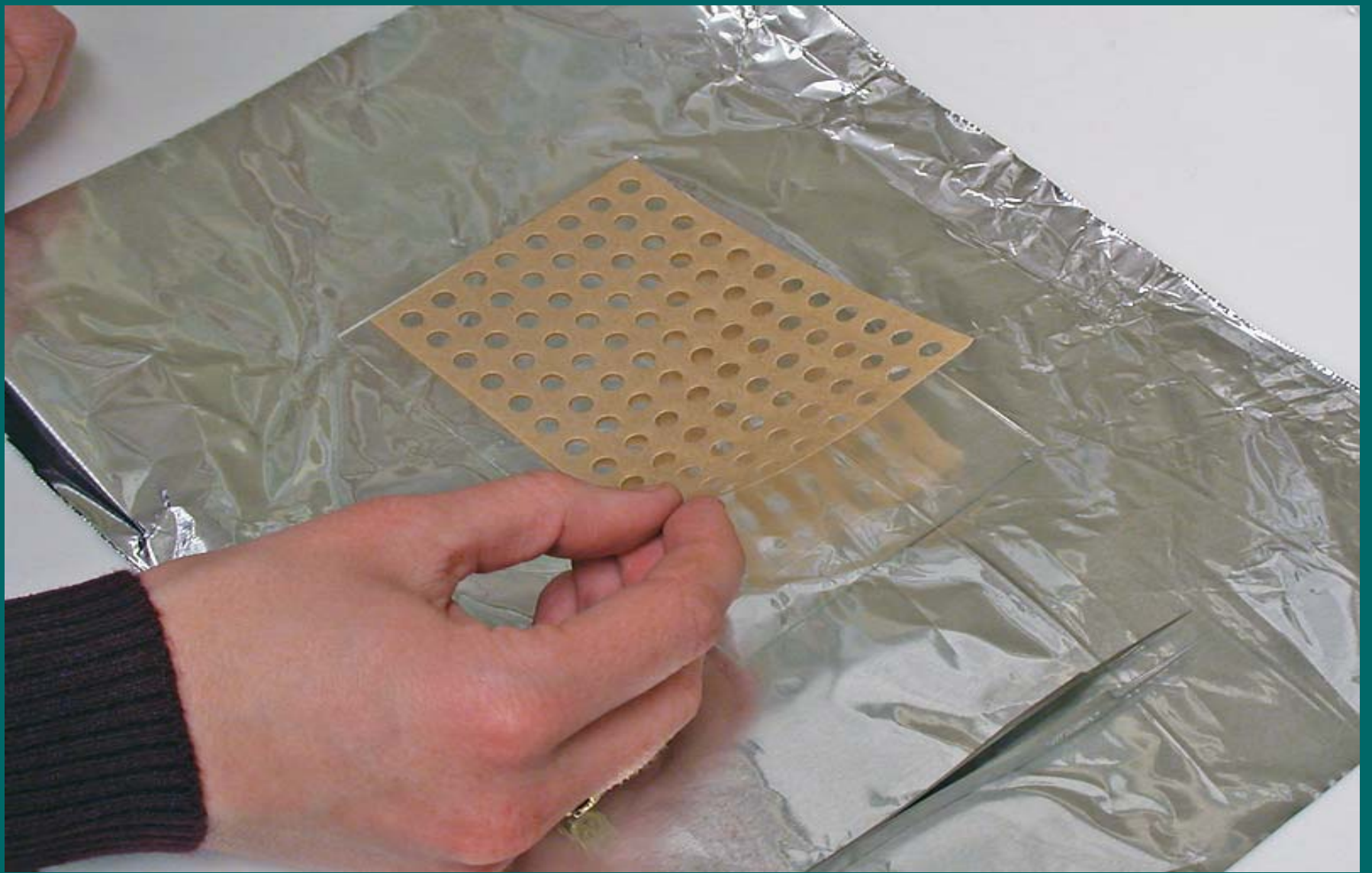
$50\ \mu\text{L} \equiv 1,000\ \text{screens}$



Cubic phase formed after mixing as can be seen in the syringe on the right hand side



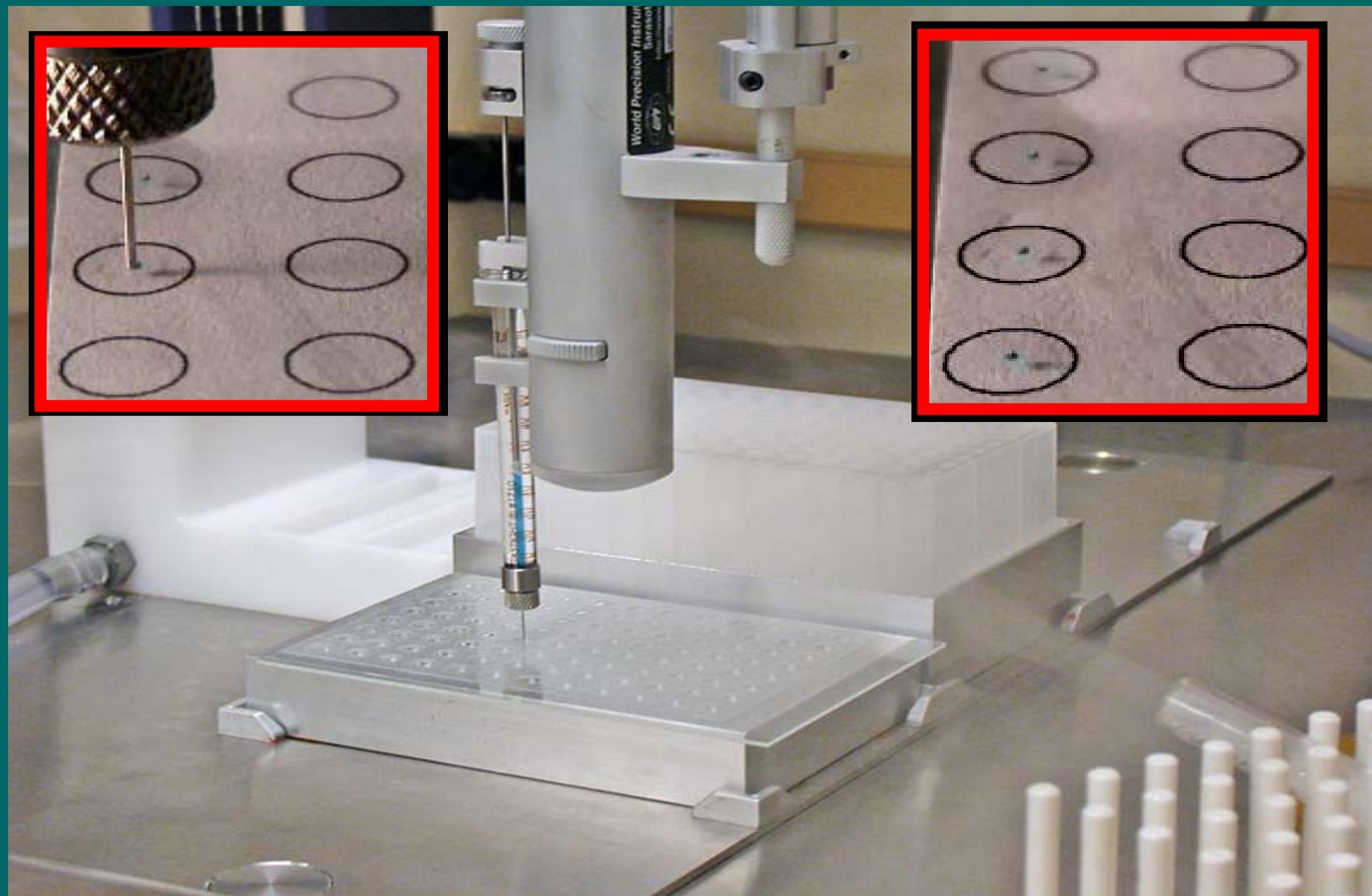
Syringe containing protein/lipid dispersion attached to automated pump on robot arm #2. Pump controller is located on the left hand side of picture.



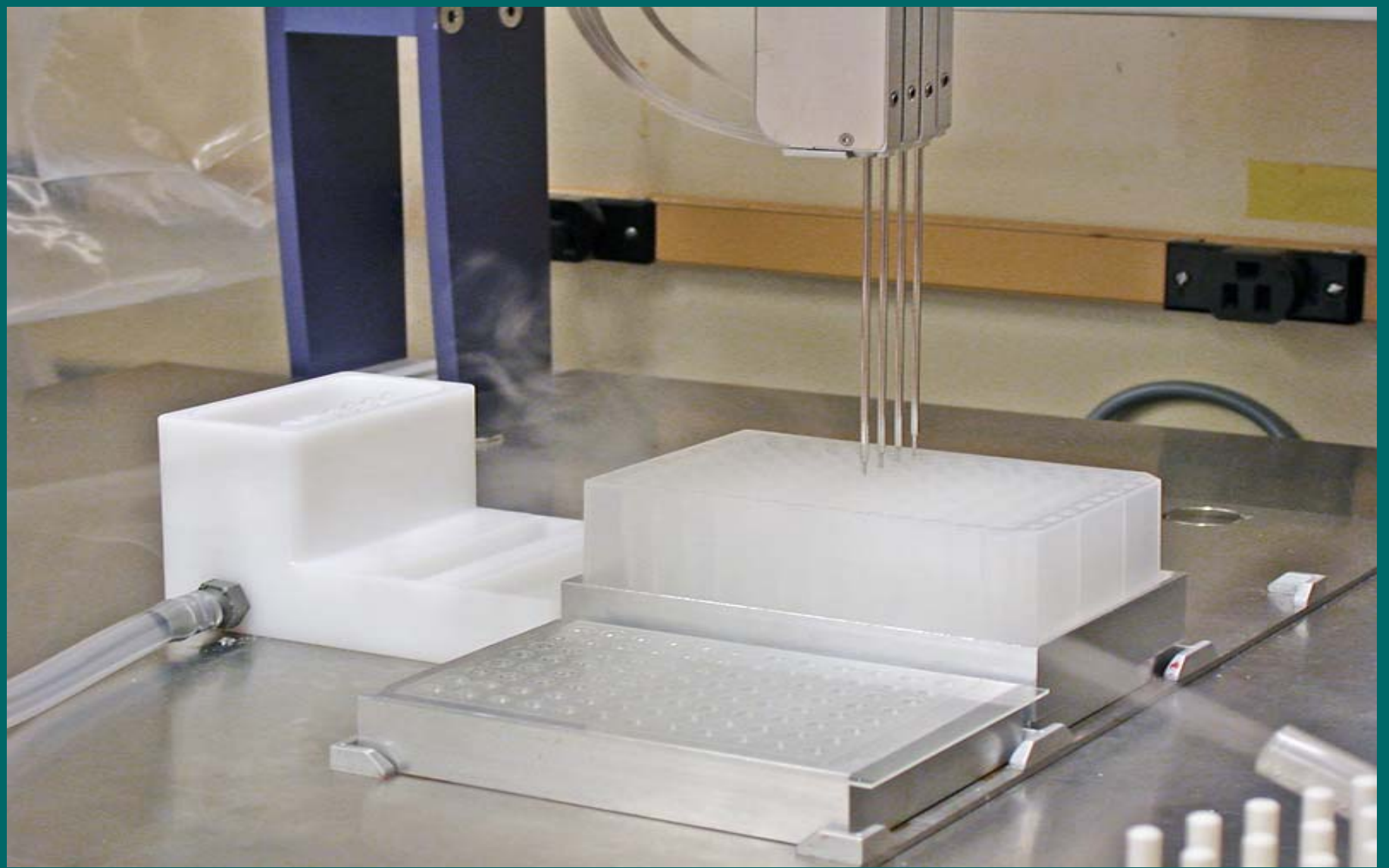
Preparation of 96-well plate: attaching perforated spacer to clean glass slide via adhesive backing



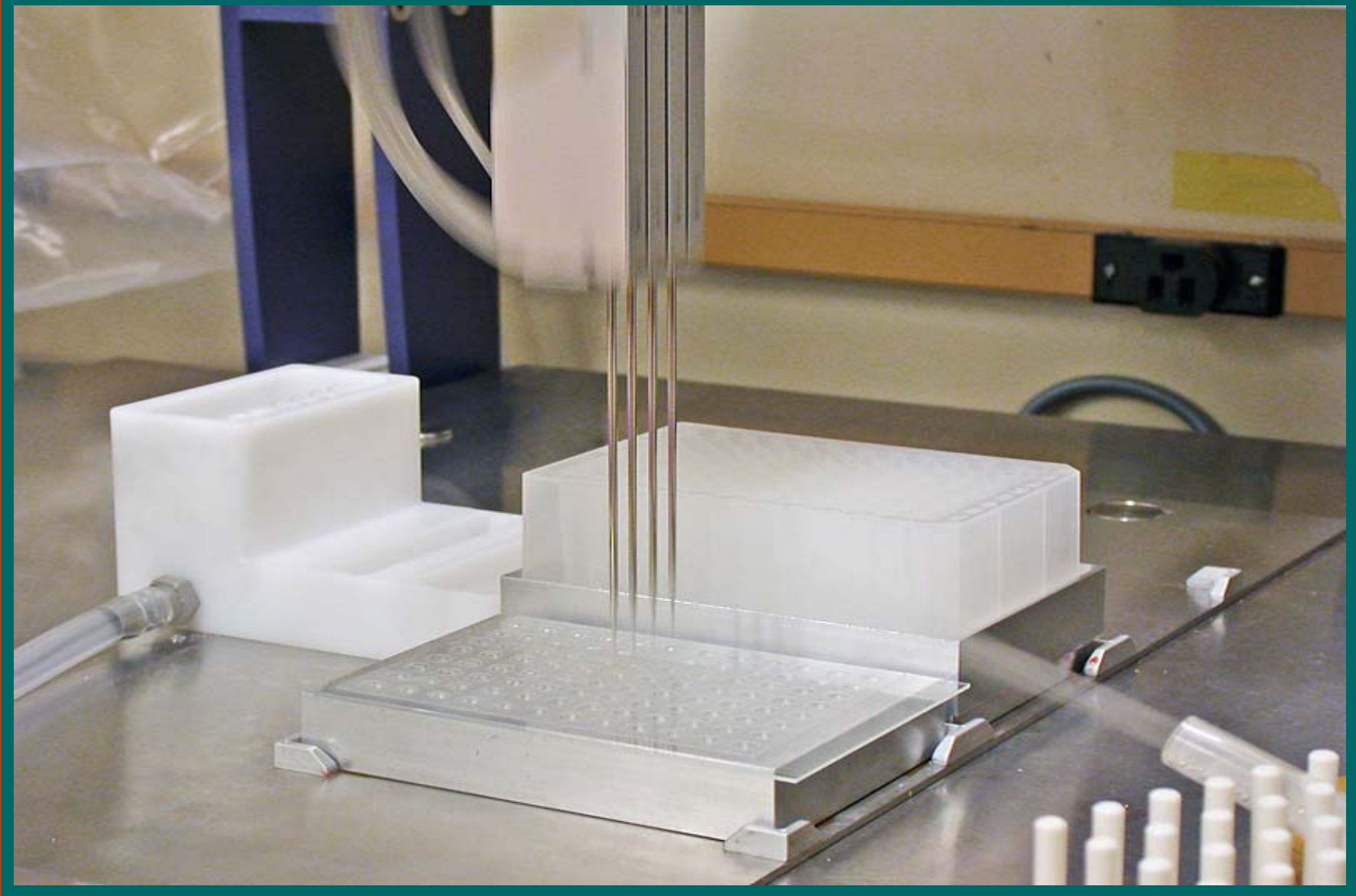
The plate/spacer is placed on the block and aligned to the imprinted template. Precipitant solutions in a 96-well block are placed in the holder behind the plate.



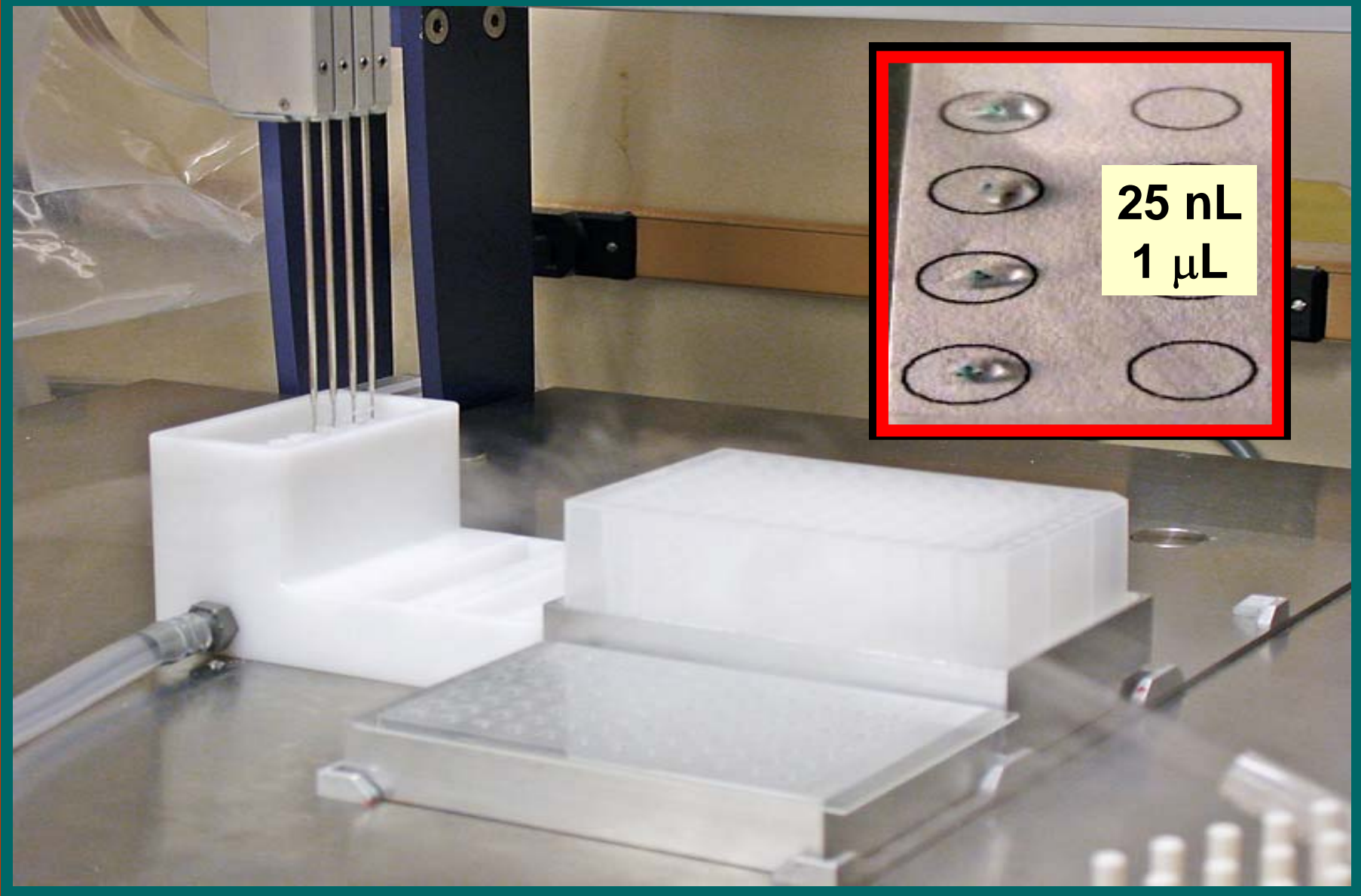
Syringe dispensing 25 nL of cubic phase into centre of well.



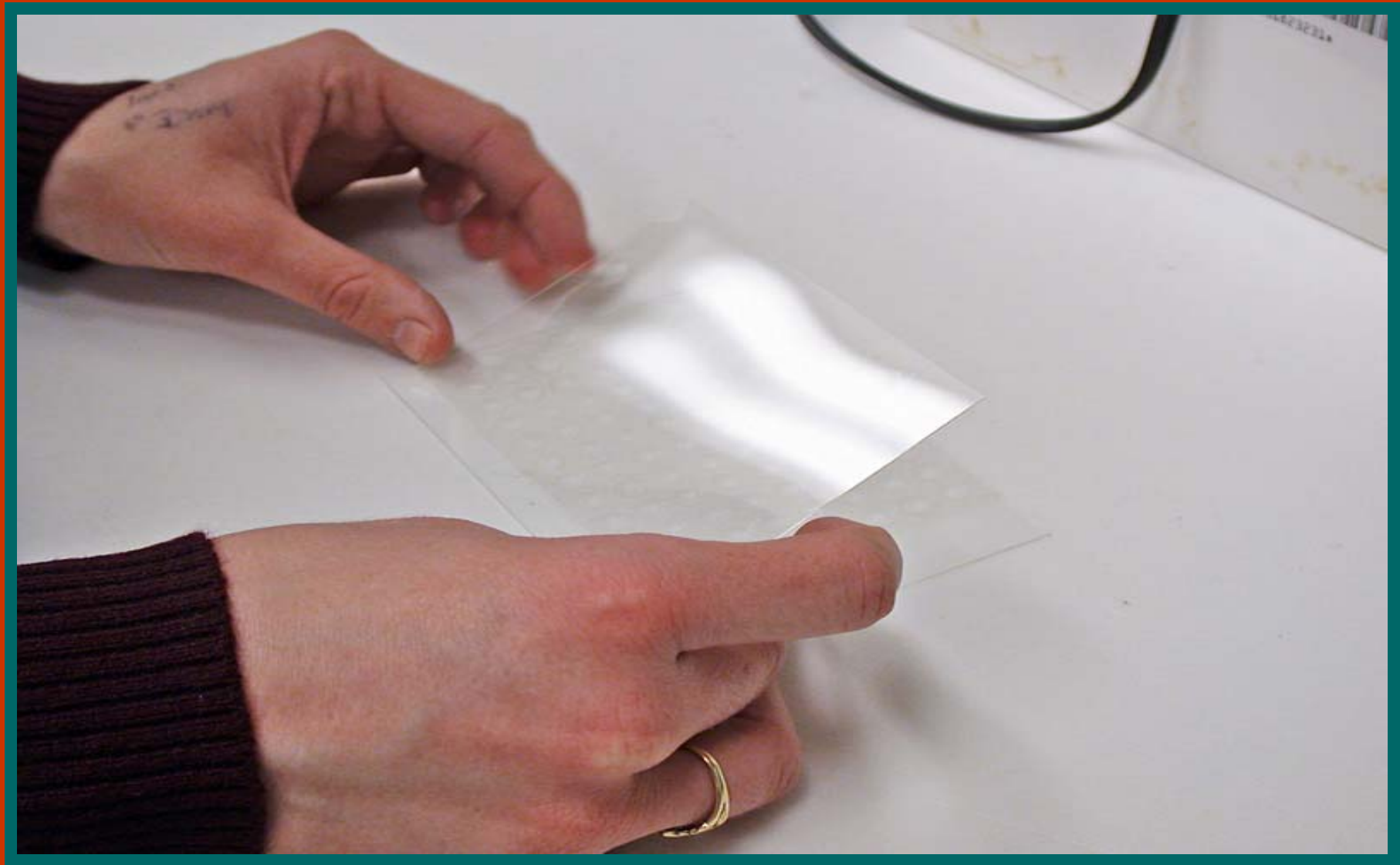
Tips on arm #1 aspirating 4 precipitant solutions from 96-well block.



Dispensing of precipitant solutions on top of cubic phase droplet in centre of well



Cleansing tips at wash station



Dispensing complete. Plate is sealed with clean glass coverslip.

A Fully Loaded and Sealed 96-well Plate

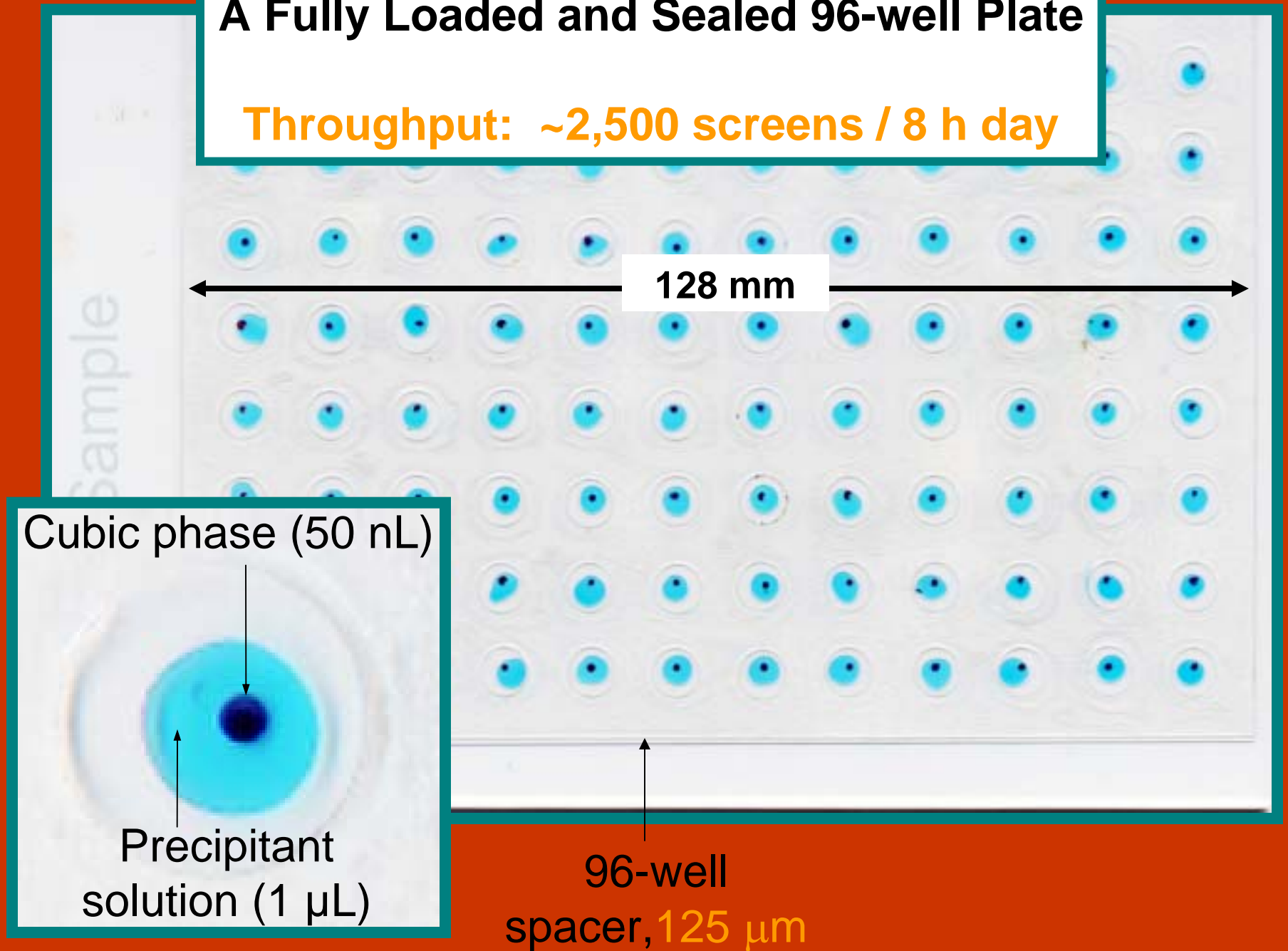
Throughput: ~2,500 screens / 8 h day

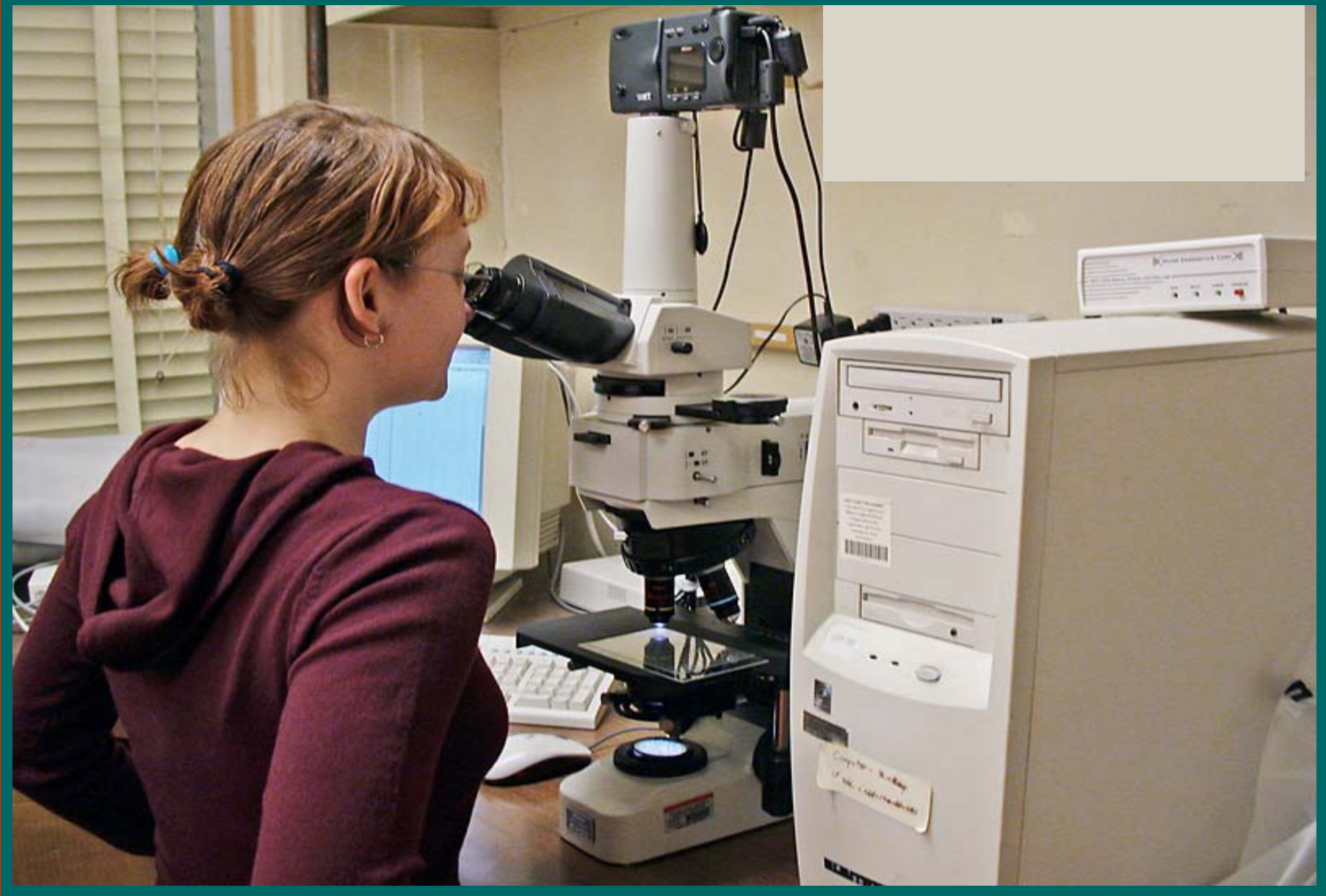
128 mm

Cubic phase (50 nL)

Precipitant
solution (1 μ L)

96-well
spacer, 125 μ m





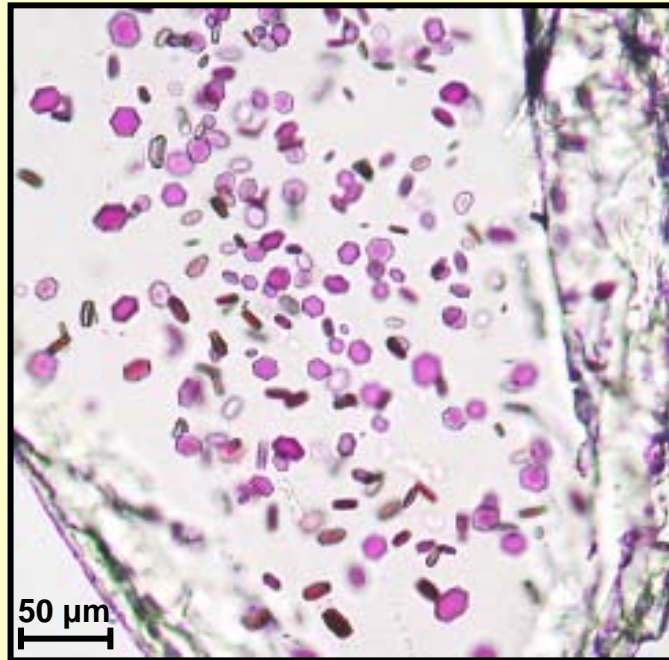
Manual viewing of wells in 96-well plate through microscope for crystal growth



Imaging robot

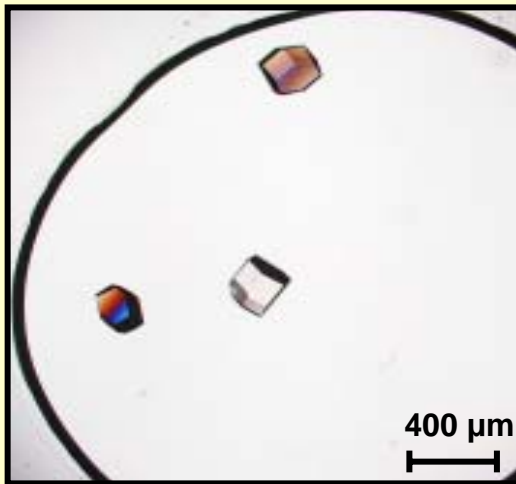
Crystals Grown Using The *In Meso* Robot: **Versatile**

A: In Meso, bR



**Plus
Economical
HTP**

B: Batch, Lysozyme



C: Bicelle, bR



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How Can APS Help ?

Small crystals, Large unit cells, High solvent content

Radiation-sensitivity

High-throughput robotic screening for diffraction quality

During screening: option to T-anneal, desiccation, etc.

***In situ* screening**

‘Fed Ex’ service. Remote evaluation of diffraction quality

Direct crystallography. 2 Å lines. S-anomalous

Standardize equipment, software and interfaces

Staffing: est. 5/beam line. BioSync Report ‘02. **Solved structures**

X-ray scattering: homogeneity, size, shape

Fast/simple access, quick turnaround, pleasant experience

ACKNOWLEDGEMENTS

Collaborators

University of Limerick
The Ohio State University

V Cherezov, Y Misquitta,
L Muthusubramaniam, A Peddi,
O Slattery, Y Zheng

Support

National Institutes of Health
National Science Foundation
Science Foundation Ireland



References

♣ Acta D. In press

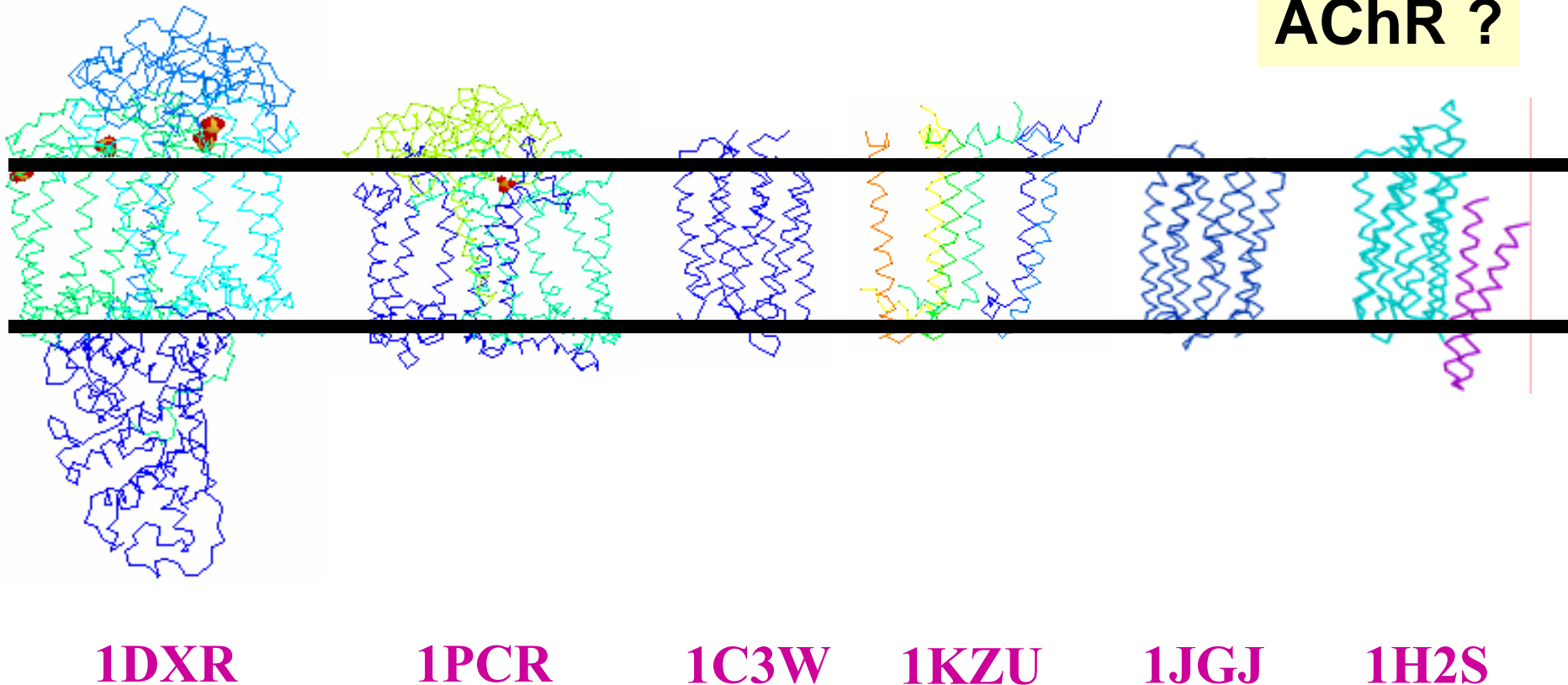
♣ J. Struct. Biol. 142: 108 - 132.

The *In Meso* Method

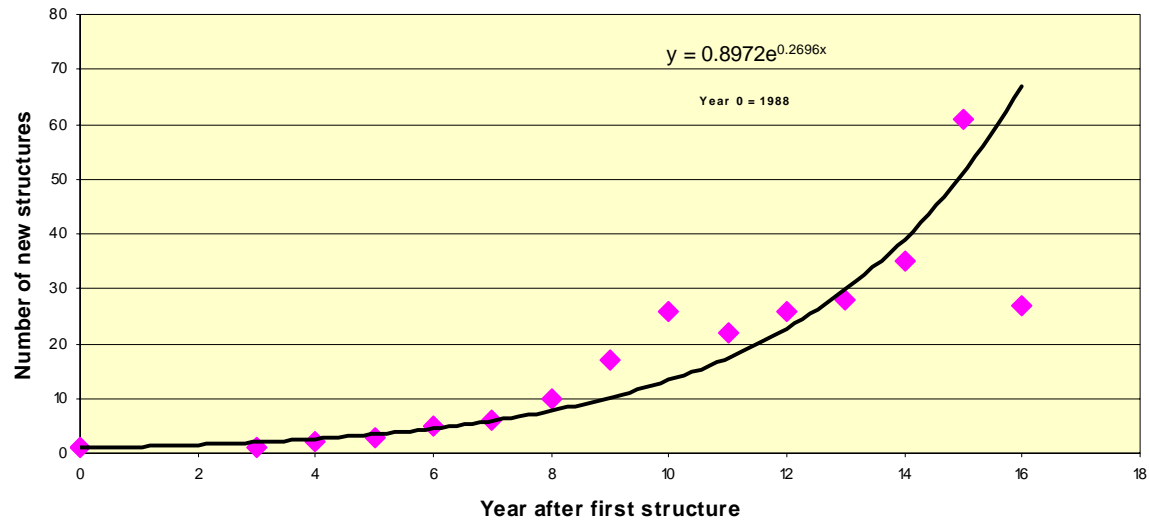
Generality

Rxn Center (*Rp. viridis*, *Rb. sphaeroides*), bR, hR, LH2, Sensory Rhodopsin II, SR II/Transducer.

AChR ?



Number of New Membrane Protein Structures Deposited
in PDB Per Year Since First Structure



Exponential Rise of New Membrane Protein Structures

